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70 His Ala Gly Thr Arg Leu Thr Gln Gly Leu Ser Asp Pro Gln Val Glu
71          15                  20                  25
73 cag ctg gcc gcc aac cac cct gac ctg cgc gcc gcc atc gac gcc gct    929
74 Gln Leu Ala Ala Asn His Pro Asp Leu Arg Ala Ala Ile Asp Ala Ala
75          30                  35                  40
77 gcc gac gaa tac gcg cgc atc aaa ccg cag gcc gcg gca ttg ctg gac    977
78 Ala Asp Glu Tyr Ala Arg Ile Lys Pro Gln Ala Ala Ala Leu Leu Asp
79      45                  50                  55
81 ctg gat gaa agc gcg cag atc gcc gcc gtg cag gat ggc ttc gtc aac   1025
82 Leu Asp Glu Ser Ala Gln Ile Ala Ala Val Gln Asp Gly Phe Val Asn
83  60                  65                  70                  75
85 ttc tat gcc gat gat gcg gtg gtg ccc tat atc gcc ctg gcc gcc cgc   1073
86 Phe Tyr Ala Asp Asp Ala Val Val Pro Tyr Ile Ala Leu Ala Ala Arg
87                  80                  85                  90
89 ggg ccg tgg gtg gtc agc ctg aag ggc gcg gtg ctg tat gac gcc ggc   1121
90 Gly Pro Trp Val Val Ser Leu Lys Gly Ala Val Leu Tyr Asp Ala Gly
91          95                 100                 105
93 ggc tac ggc atg ctc ggc ttc ggc cat acc ccg gcc gat atc ctg gag   1169
94 Gly Tyr Gly Met Leu Gly Phe Gly His Thr Pro Ala Asp Ile Leu Glu
95          110                 115                 120
97 gcg gtc ggc aag ccg cag gtg atg gcc aac atc atg act ccc tcg ctg   1217
98 Ala Val Gly Lys Pro Gln Val Met Ala Asn Ile Met Thr Pro Ser Leu
99      125                 130                 135
101 gcc cag ggc cgc ttc att gcc gca atg cgc cgc gaa atc ggc cat acc  1265
102 Ala Gln Gly Arg Phe Ile Ala Ala Met Arg Arg Glu Ile Gly His Thr
103 140                 145                 150                 155
105 cgc ggc ggc tgc ccg ttc tcg cac ttc atg tgc ctg aac tcc ggc tcc  1313
106 Arg Gly Gly Cys Pro Phe Ser His Phe Met Cys Leu Asn Ser Gly Ser
107                 160                 165                 170
109 gaa gcg gtc ggg ctg gcc gcg cgc atc gcc gac atc aac gcc aag ctg  1361
110 Glu Ala Val Gly Leu Ala Ala Arg Ile Ala Asp Ile Asn Ala Lys Leu
111                 175                 180                 185
113 atg acc gac ccg ggc gcc cgg cat gcc ggc gcc acg atc aag cgc gtg  1409
114 Met Thr Asp Pro Gly Ala Arg His Ala Gly Ala Thr Ile Lys Arg Val
115         190                 195                 200
117 gtg atc aag ggc agt ttc cac ggc cgt acc gac cgt ccg gcg ctg tat  1457
118 Val Ile Lys Gly Ser Phe His Gly Arg Thr Asp Arg Pro Ala Leu Tyr
119     205                 210                 215
121 tcc gat tcc acc cgc aag gcc tac gat gcg cat ctg gcc agc tac cgc  1505
122 Ser Asp Ser Thr Arg Lys Ala Tyr Asp Ala His Leu Ala Ser Tyr Arg
123 220                 225                 230                 235
125 gac gag cac agc gtc att gcc atc gcc ccg tat gac cag cag gcc ctg  1553
126 Asp Glu His Ser Val Ile Ala Ile Ala Pro Tyr Asp Gln Gln Ala Leu
127                 240                 245                 250
129 cgc cag gtg ttt gcc gat gcc cag gcc aac cac tgg ttc atc gag gcg  1601
130 Arg Gln Val Phe Ala Asp Ala Gln Ala Asn His Trp Phe Ile Glu Ala
131             255                 260                 265
133 gtg ttc ctg gag ccg gtg atg ggc gaa ggc gac ccg ggc cgt gcg gtg  1649
134 Val Phe Leu Glu Pro Val Met Gly Glu Gly Asp Pro Gly Arg Ala Val
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135        270                 275                 280
137 ccg gtg gac ttc tac cgc ctg gcc cgt gag ctg acc cgc gaa cac ggc   1697
138 Pro Val Asp Phe Tyr Arg Leu Ala Arg Glu Leu Thr Arg Glu His Gly
139    285                 290                 295
141 agc ctg ctg ctg atc gat tcg atc cag gcc gcg ctg cgc gtg cac ggc   1745
142 Ser Leu Leu Leu Ile Asp Ser Ile Gln Ala Ala Leu Arg Val His Gly
143 300                 305                 310                 315
145 acc ctg tcc ttc gtc gac tac ccc ggc cac cag gag ctg gag gca ccg   1793
146 Thr Leu Ser Phe Val Asp Tyr Pro Gly His Gln Glu Leu Glu Ala Pro
147                 320                 325                 330
149 gac atg gag acc tac tcc aag gcc ctg aac ggc gcc cag ttc ccg ctg   1841
150 Asp Met Glu Thr Tyr Ser Lys Ala Leu Asn Gly Ala Gln Phe Pro Leu
151            335                 340                 345
153 tcg gta gtg gcc gtg acc gag cac gcc gcc gcg ctg tac cgc aag ggc   1889
154 Ser Val Val Ala Val Thr Glu His Ala Ala Ala Leu Tyr Arg Lys Gly
155        350                 355                 360
157 gtg tac ggc aac acc atg acc acc aac ccg cgg gcg ctg gac gtg gcc   1937
158 Val Tyr Gly Asn Thr Met Thr Thr Asn Pro Arg Ala Leu Asp Val Ala
159    365                 370                 375
161 tgc gcc acc ctg gca cgc ctg gat gag ccg gtc cgc aac aat atc cgc   1985
162 Cys Ala Thr Leu Ala Arg Leu Asp Glu Pro Val Arg Asn Asn Ile Arg
163 380                 385                 390                 395
165 ctg cgt ggc cag cag gcg atg cag aag ctg gaa gca ttg aag gaa cgg   2033
166 Leu Arg Gly Gln Gln Ala Met Gln Lys Leu Glu Ala Leu Lys Glu Arg
167                 400                 405                 410
169 ctg ggg ggc gcg atc acc aag gtg cag ggc acc ggc ctg ctg ttc tcc   2081
170 Leu Gly Gly Ala Ile Thr Lys Val Gln Gly Thr Gly Leu Leu Phe Ser
171            415                 420                 425
173 tgc gag ctg gcc ccg cag tac aag tgc tac ggg gcc ggc tcc acc gag   2129
174 Cys Glu Leu Ala Pro Gln Tyr Lys Cys Tyr Gly Ala Gly Ser Thr Glu
175        430                 435                 440
177 gag tgg ctg cgc atg cac ggg gtc aat gtg atc cac ggc ggc gag aat   2177
178 Glu Trp Leu Arg Met His Gly Val Asn Val Ile His Gly Gly Glu Asn
179    445                 450                 455
181 tcg ctg cgc ttc acc ccg cac ttc ggc atg gac gag gcc gaa ctg gac   2225
182 Ser Leu Arg Phe Thr Pro His Phe Gly Met Asp Glu Ala Glu Leu Asp
183 460                 465                 470                 475
185 ctg ctg gtg gag atg gtc ggg cgt gcg ctg gtc gaa ggc cca cgc cgg   2273
186 Leu Leu Val Glu Met Val Gly Arg Ala Leu Val Glu Gly Pro Arg Arg
187                 480                 485                 490
189 gcc tga tccgcacccg caggacggaa ggcacgagcc caccgtgagg cgggctcttt gc  2331
190 Ala
192 tgcccggcac cagcggcaac aggccgcgct gtcaccggcc aggcggggcg ccggcagtgg  2391
194 gtttcagccg caggggtccg ccctgccagc gcctgcggcg gggcacaggc ttgcgggcat  2451
196 tgcggcctct gccacgggca cgcagccgga gatcaggctg acaagggggc tgccccgggt  2511
198 ggcagtacac gaccagccag ttgactgccg gtatttgctt gatcagcgct gcatccagaa  2571
200 cagcaccatc ggttgcgtga ctgacgcgcc gctggccgtt gcgggacagc agcctttgcg  2631
202 tcacacgtgg cccgcacctg cctgcactgc ag                                 2663
204 <210> SEQ ID NO: 2
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RAW SEQUENCE LISTING   DATE: 04/04/2003
PATENT APPLICATION: **US/09/762,230A**   TIME: 14:23:29

Input Set : **A:\FUJII Sequence listing (.txt**
Output Set: **N:\CRF4\04042003\I762230A.raw**

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205 <211> LENGTH: 6357
206 <212> TYPE: DNA
207 <213> ORGANISM: Flavobacterium lutescens
209 <220> FEATURE:
210 <221> NAME/KEY: CDS
211 <222> LOCATION: (2855)..(4387)
213 <400> SEQUENCE: 2
214 ggatcgggcc actgggctca ctgctggacg caatccgagt gccgggatgg ctcgggttga 60
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218 gcaccacctt ggcgccgaaa taggccagtt cgcaggcctc gtcatagctg agcgtggcca 180
220 gggtcaccgc ctcgggcacc acccgcgggt cggccgacag cacaccgtcg acatcggtcc 240
222 agatgtgcag ctcggccgcc tcgaacagcg cggcaaagat cgccccggaa taatcgctgc 300
224 cgttgcggcc caggtggtg atcctgccct ggccatcacg ggcgacaaaa ccggtgacca 360
226 ccacccgcga ctgcgggttg tccacacgcc aggcggccag gttggccgca ctgcgttccc 420
228 agtcgacgct gacccccagc tcgccgtgtg cgaccaccag cacatcgcgg gcatcgagca 480
230 ccgcgcaggg gtggccgagc cggttgaaat agcggcccag cagctgggcc gagaacacct 540
232 cgcccagccc ctgcaccctt tcaagcacct cctcgggcag gccgccgatc accgccagcg 600
234 cttccagcaa cccggccagc ttgtcaaagc gtccatccag ccactgcagc aggtcggcag 660
236 aatcctcgcc cagcagttcg gtggccgctt catggtggcg ctggcgcagg gcctgccagg 720
238 catcacgcca gcgcggctga ccgtgggcgg ccaggtagc cagctcgatc aaggcatcgg 780
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242 actcggcgac atggcggtag cgctgcgccg aggccaccga ggtgccgccg aacttgtggg 900
244 cgatgacctg ggcatcgggc gcgggagcgg gagcgggtgc agcggcaggc gatgacatca 960
246 caacagacct ctggggttga ggcccggcac cgcaggttgc gaagtcccgc aacctggtcg 1020
248 gtgcgggggcc gttgtttttcg ggggttagac gaatacgacg ggccgcacca gccaagtggt 1080
250 ggtggtaatg atggtcatgc cggtgacgcc agcaggcgcc agcagggcgg cagtggaatc 1140
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254 ctgttgcatt gcaaaataat tttccgcgca tcatcggcga acatgcaccg atttggttgc 1260
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294 atgaacaaca ggccggggcg cgcagcgca tgggcgctgg cagctctccg acctgtgcaa 2460
296 aggtggtggc cccgacacga ttcgaacgtg cgacctgtcc cttaggaggg gaccgctcta 2520
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298 tccagctgag ctacggagcc atgaggccgg cgattctagc atccgctctc cgttcacggc 2580
300 catcgcccgc agccgcagtt cacagtgcag ggcaaccgca gcaagccccc gccccgctgc 2640
302 aaccctcgcg cccgcgcgca acgtgaccgg cgccgcggca ggcccggccc ccacggccac 2700
304 tggcgccggt tccgcaccac gccaccggca acacgccccc agccctgccc aacgtggtgt 2760
306 ttcagcgctc tgttaagatg gcatgcccac atgccacctc cccccggacg cgccgcgggt 2820
308 gcgtgacctt ttcgtaacgt aatctggagt ttcc atg tcg ttt gaa ctg ctc aag 2875
309                                    Met Ser Phe Glu Leu Leu Lys
310                                     1             5
312 gcc tta ggg ctg gac gcc acc aat tcc ggc acc tac ctg ggt gat gga 2923
313 Ala Leu Gly Leu Asp Ala Thr Asn Ser Gly Thr Tyr Leu Gly Asp Gly
314          10                  15                  20
316 gaa tgg tcc agc gct acc ggt gcc ggg acc atc agc ccg cgc aac ccg 2971
317 Glu Trp Ser Ser Ala Thr Gly Ala Gly Thr Ile Ser Pro Arg Asn Pro
318      25                  30                  35
320 acc acc ggc gag gtc att gcc cag gtc cag gcc acc acc gag gcg gac 3019
321 Thr Thr Gly Glu Val Ile Ala Gln Val Gln Ala Thr Thr Glu Ala Asp
322 40                  45                  50                  55
324 tac gaa acc atc ctg gcc cgc gcc cag cag gcc ttc aag gtc tgg cgc 3067
325 Tyr Glu Thr Ile Leu Ala Arg Ala Gln Gln Ala Phe Lys Val Trp Arg
326                  60                  65                  70
328 acc acc ccg gca ccg cgc cgc ggc gag gcc atc cgc ctg tgt ggc gag 3115
329 Thr Thr Pro Ala Pro Arg Arg Gly Glu Ala Ile Arg Leu Cys Gly Glu
330                  75                  80                  85
332 gcc ctg cgc cgc cac aag gac gcg ctg ggt tcg ctg gtc gcg ctg gaa 3163
333 Ala Leu Arg Arg His Lys Asp Ala Leu Gly Ser Leu Val Ala Leu Glu
334          90                  95                  100
336 atg ggc aag tcc aag ccg gaa ggc gac ggc gaa gtc cag gaa atg atc 3211
337 Met Gly Lys Ser Lys Pro Glu Gly Asp Gly Glu Val Gln Glu Met Ile
338      105                 110                 115
340 gac atc gcc gac ttt gcc gtc ggc cag agc cgc atg ctg tat ggc tac 3259
341 Asp Ile Ala Asp Phe Ala Val Gly Gln Ser Arg Met Leu Tyr Gly Tyr
342 120                 125                 130                 135
344 acc atg cac agc gag cgc ccc ggc cac cgc atg tac gag cag tac cag 3307
345 Thr Met His Ser Glu Arg Pro Gly His Arg Met Tyr Glu Gln Tyr Gln
346                 140                 145                 150
348 ccg ctg ggc atc gtc ggc atc atc tcg gcc ttc aac ttc ccg gtc gcg 3355
349 Pro Leu Gly Ile Val Gly Ile Ile Ser Ala Phe Asn Phe Pro Val Ala
350              155                 160                 165
352 gtc tgg gcc tgg aac agc ttc ctg gcc gcg atc tgt ggt gat gtc tgc 3403
353 Val Trp Ala Trp Asn Ser Phe Leu Ala Ala Ile Cys Gly Asp Val Cys
354          170                 175                 180
356 atc tgg aag ccg tcc aac aag acc ccg ctg acc gcg atc gcg tcc atg 3451
357 Ile Trp Lys Pro Ser Asn Lys Thr Pro Leu Thr Ala Ile Ala Ser Met
358      185                 190                 195
360 cgc atc tgc aac gaa gca ctg cgc gaa ggc ggc ttc ccg gac atc ttc 3499
361 Arg Ile Cys Asn Glu Ala Leu Arg Glu Gly Gly Phe Pro Asp Ile Phe
362 200                 205                 210                 215
364 ttc ctg atc aac gac gcc ggc acc gcg ttg tcg gag aag ctg gtc gag 3547
365 Phe Leu Ile Asn Asp Ala Gly Thr Ala Leu Ser Glu Lys Leu Val Glu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/04/2003
PATENT APPLICATION: **US/09/762,230A**   TIME: 14:23:30

Input Set : **A:\FUJII Sequence listing (.txt**
Output Set: **N:\CRF4\04042003\I762230A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 6,9,12,15,18,21,27,30
Seq#:9; N Pos. 3,9,12,15,18,21,24,27,30

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 13,15,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36
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US 0976223007P1

Creation date: 12-23-2003
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Legal Date: 04-08-2002

No.	Doccode	Number of pages
1	M903	2

Total number of pages: 2

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